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RESULT 1
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LOCUS
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
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                      TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and is derived by analysis of the total score distribution
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                                                                                                                  Cole,S.T., Brosch,R., Parkhill,J., Garnier,T., Churcher,C., Harris,D., Gordon,S.V., Eighmeier,K., Gas,S., Barry III,C.E., Tekaia,F., Badcock,K., Basham,D., Brown,D., Chilingworth,T., Connor,R., Davies,R., Devlin,K., Feltwell,T., Gentles,S., Hamlin,N., Hoiroyd,S., Hornsby,T., Jagels,K., Krogh,A., McLean,J., Moule,S., Murphy,L., Oliver,S., Osborne,J., Quail,M.A., Moule,S., Murphy,L., Oliver,S., Seger,K., Skelton,S., Seger, K., Skelton,S., Skelton,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis
Eubacteria; Firmicutes; Actinomycetes; Mycobacteria;
Mycobacteriaceae; Mycobacterium.
                                                                               Squares, S., Sqares, R., Sulston, J.E., Taylor, K., Whitehead, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis
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Deciphering the biology of Mycobacterium tuberculosis from the
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12732
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /home/sdavid/sdavid-tmp/may03/chakrabarti476/AL123456.gbk:*/home/sdavid/sdavid-tmp/may03/chakrabarti476/AEC00516.gbk:*
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ACCESSION: AL123456
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Sabmitted (i1-JUN-1998) Submitted on behalf of the Myorobacterium
Elberculosis sequencing and mapping leads. Sanger Centre, Wellcome
Trust Senore Campus. Binxton, Cambridge CBi0 ISA Unite de Genelique
Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux,
75724 Paris Cedex IS, France E-mail: parkhillssanger.ac.uk
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98295987
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                                                                                                                                                                                                                                                                                                           /protein_id+"CAA16239.1"
/brotein_id+"CAA16239.1"
/db_xxet-"31:32615.3"
/db_xxet-"31:02615.3"
/translation-"mdha/tryushunterllresfalayswyaknipakeaypyisg
vlltgsdnglfisgfdyersabaywgabivsposylvsgrilsi-phealekkpyiwhy
vlltgsdnglfisgfdyersabayygabivetheeff3llpabifakeafsgvataaghddi
vww.coxxuunterllresfalaysgribytheffpeff3llpabifakeafsgvataaghddi
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                                                                                      LPMCTGTRYELIGETYVLAATDRERLAYRELKWSASSPOLBAAYLYPÄKTLAEAAKAG
IGSSEVRISIGTGPGYGKIGLIG ISGNEKRITTILIGAEFEREPGLYTYTEITTAVALMI
VAEILIEAIKIVALVADRGAGVEKEFAGKERITTILIGAEFEREPLYVYYTGEPLITA
FNOTYLTDGLSSLRSERVSFGFTTAGKFALLRPVSGDDRPVAGLMANGPFPAVSTDYV
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/product-"dnaA"
/protein_id="CAA16238.1"
/db_xref="GI:2808711"
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ATP/GIP-binding site notit A (P-loop) and PSJ1008 Thak protein signature. Note that the first base of this gene
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/db_xref-"taxon:1773"
                                                         CLIMPVREPG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="dnaN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hase been taken as base 1 of the M. tuberonlosis Higher
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /qese="dnaA"
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/note-*RvC003, (MTCY10H4.51), recE gene, len: 385, TR:E208998; contains PS00017 ATP/GTP-binding site motif A, PS00617RecE protein signature 1, PS00618 RecE protein signature 2*
                                                                                                                                                                                                                                                                                                                                                                                     SSAQARTAAAKAPELVRKSATDTGGLEGKLÅDCRSTÖPRKSELYVVEGDSAGGSAKS
GRUSMFQAILFLEGKTINVEKAKLDRVLKNTEVGAIITALGTGIHDEFDIGKLRYHKI
VLMAPADVDSGHISTLLIILGHEMRPLIENGEVELAGPPLYKLKNGRSDFEFANSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KRAQDEYGAAS I LILEGJEAVRKHERMY I GSTGERGLIHHLIMEVYDNAYDEAMAGYĀI
TVNVVLLEDGGVEKADGGKO TRVAI HASSI J PYÖDVANTQLIAGAGKERGSAXAI SGGLI
HADGS KRAI SKRINGERS KRAI SKRING KRAI SKRING KRAI SKRING
KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING KRAI SKRING
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/*ranslation="MYVRHLGLRUFRSWACVDLRLHPGRTVFVGPNGYGKINLIRALWYSTHGSHRYSADLPLHRYGTUGAVISTVVNNCRECAVDELATGRVNKARLNRSSV
                                                                                                                                                                                                                                                                                  ADELFSILMGSUVDABRSFITRNAKDVRFLDV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GYSESVHTFANTINTHEGGTHEEGFRSALTSVVNKYAKDRKLLKDKDPNLTGDDIREG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product-"gyr8"
/protein_id="CAB02426.1"
/db_xref="GI:1552558"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KITGPAAPSWRKGPRHIAGRGPRDTYG"
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RGRVASVASGRVAGRRKKSWSGPGPDIRDPGFLGKAARELAKKRGWSVRVAEGMVLGGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="hypothetical protein Rv9004"
/protein_id="CAB02425.1"
/db_xref="GI:1552557"
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to ORE187 in recF region, MTOKIREP_6, E238999 (187 aa)
(97.9% identity in 187 aa overlap)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4434.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RSTROVOVUKAVLFAPRILGIJVRGDIADRRHYLDILATVRRPATÄÄVJAEYENVLÄO
KTALLKSVEJARYKGDROVEDTLEVMÖSRLÄNNIGAET VAAKLIJVAUGLA PEVKKAYOL
LAPEERSASS GYRASMITVIGPSEROSILEROLLANGARLIJAALAARROAFLEROKUTYGH
RDDILLERJONGRAKGFANHGEAMSLAVALKLAAYOLLRVDGGEPVLLILDIVFAELIUM
                                                                                                                                                                                                                                                                                                                                                      ERDGILLEAGIKAGKKI NKEDGI QRYKGI GEMDAKEI NET IMDPSVRVILRQVII DDAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAAVISVKVSEPQFEGQIKTKLGNTEVKSFVQKVONEQLIHWFEANPTDAKVVVVNKAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AESTAPHKVKSRTFHYPGHLVDEVKHINRTKNAIHSSIVDESGKG1GHEVEIAMOWWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /hote-"Rv0005. (MTCY10H4.03), gyrH, dna gyrase subunit h.
len: 714. identical to GYRB_MYCTU P41514, contains PS0017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /transi_table=11
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/db_xref="EMBL:3261645"
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3280..4437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start-1
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/db_xref="GI:1552556"
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                                                        /db_xref="EMBL:3261645"
                                                                                                                /note-"kv0006"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MCKNEARRSALAPDHGTVVCDPLRRLNRMHATFEESIRlVAACK
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302..9818
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Db 1696435 TOGGCACCASCTGGTCAAACGCCAACGCCTCCCCCTTCCCCCATCGACGCCCC [696494
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                                                                                                                                                                                                                           Db 1696375 GTAGAGCCCCATAGCCACAGCCTAGATCGTTGATCGAAAATGGGTCCGCCGCATTGACAA 1696434
                                                                                                                                                                                                                                                                                                                                                                                Db 1696315 CGGGGGAGACGTCGATGCCGGTGTAATCAGTTTTGAAGCCACGCGCATCTAGGTAGTCCA 1696374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db 1696255 CSCAGAIGAAGICTGCGTTCGCCCGACCITCGAAACGTAGIGCGGCCGCGCGCACCATTT 1696314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 1696075 TOTTTGATGCATCGGAATAAGATGTCAGGCAATTAAAAGAGAAACCCACGGCGACTCGCGG 1696134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db 1596015 ACCTSCSCTTGCAGAGATCAAATAGGGCSCATGGGTCAGCATAGTACAGGTCGTCGCCCA 1696074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 12732;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 GGCAGATSAAGTCTSGGTTCGGCCGACCTTCGAAACGTAGTGCGGCGCGCGCGCACCATT 3/6
481 GUSSGTGCCGTGTGGTTCGAGTTTCGATGCGTAGTAACGGGCCACGTCAGCGAGCATCGT 540
                                                                                                                                                 421 TGOSCACCAGCTGGTCAAAAGCGCAACGCCTGCCCGGCTTCGCCGTTCCAATGGACGCCGC 480
                                                                                                                                                                                                                                                                  361 GIAGASCOCCATAGCCACASSCIAGATEGITGAJEGAAAATGGGTECGCCCATTGACAA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 CGGGGAGACGTCGATGCCGCTGTAATCAGTTTTGAAGCCACGCGCATCTAGGTAGTCCA 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 GACGAACATTGAATATTCCACTCGCGACGCTATAGTCCGCCTCCCGATCTATGCGCGCCC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 CATTOMSCATSTCGASCGTCGCTTCGATGTGAGCGCACCATTCCGTGTCCAACGATTTCA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 TOTTTSATGCATCGGAATAAGATGTCAGGCAATTAAAAGAGAAAGCCACGGCGACTCGCGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     i ACCTGCGCTTGCAGAGATCAAATAGGGCCCATGGGTCAGCATAGTACAGGTCGTCGCGCA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    //note="Re0007 (MTCY10H4.05), len: 304. Unknown but
similar to 270722|MLCB1770_7 Mycobacterium Leprae cosmid
B1770 (303 aa), FASIA scores: opt: 812 z-score: 593.0 E():
1.6e-25. 54.2% identity in 319 aa overlap*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DLIAREDYVVTITTETGYAKRTKTDDYRSQKRGGKGV<sub>Y</sub>JAGLK<sub>Y</sub>DDIVAHFIV:STHUL
TLFFTTQGRVYRAKAYDLPEASRTARGQHVANLLAFQPEERIAQVIQIKGYTDAPYIV
LATRNG_VKKSKLTDEDSNRSGGIVAVNLRUNDEIJVGAVLCSAGUULLIVSANGGSIK
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31.WKALDALDEVYALTRASETVDTARAGLTELLDTDETQAQAT;.DMGLRRLAALEROR
TIDDLAK:EARTADLEDTLAKPERORGTVRDELAETVURHGDDHRTRTTAADGDVSCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QEPTVLPSRFPNLLANGSGGIAVGMATNIPPHNLRELADAVFWALENHDADFEETLAA
WMGRVKGPDFPTAGLIVGSQGTADAYKTGRGSIRMRGVVEVEEDSRGRISLVITELPY
QVAHDUNFITSIAEQVRDGKLAGISNIEDQSSDRVGLRIVIEIKRDAVAKVVINNIYKH
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WSLRYPLVDGQGNFGSPGNDPPAAMRYTEARLTPLAMEHLREIDEETVDETPNYDGRV
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/protein_id="CAB02427.1"
/db_xref="GI:1552559"
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ps00318EF-hand calcium-binding domain*
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QY 1441 SOSCOSOGACAGOTOCOCTOGAGOGACTTCAAGGGATTCTGGGACATATTCAATATGGT 1800 DE 1697455 SOGCOCGGGACAGOTCCGOTGGAGOGAGTTCAAGGGATTCTGGGAGAGATTCAATATGGT 1897514
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Eb 1697275 CTCGITTGAICCGATTCTGTITTCGCCCAAFCACGCTTGGTATATTGCATGTCATCATAG 1697334
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                                                          1381 GATTSAACAATGGCGACTTTGTTGAACGCGGTGTCTCCAATTTAGAATAACAAATACGTC 1440
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Qy 2581 AGCAACAGAATGGGGACGACGAGGGGGATACGGGGTCCGAGGGCGCAGGACGGGAGC 2640 H.: - - - - - - - - -
Qy 2521 GGCAAGACGAAAACGAGAFAGTAGAAGGCGACGTCCGGGGGGGAGAAGGTGGCGGTGGGG 2580 H H F H F H H H H H
Qy 2461 TGGTCGAATATCCCAGCACCAGGAGGCCCGTTGGGGTCTCGGGCTACCAGTGCAGCGAFT 2520 HTT: HTT: HTT: HTT: HTT: HTT: HTT: HTT
9y 2401 GCCACGGCAAACTSACGCAGACGCCGACGGGGGGGGGGGG
OY 2341 TGTCCATAGASCSGCACGTAGAACGGCTSGCCGGGGACGCGACGTTGACGATGCTSAS: 2400
Oy 2281 GODGATGTCACCGTGGTGAAAACGAGTGGCGTGGTACCGACTACCCCTTTGGCTCCCAGC 2340 I III : IIII : IIII IIII IIII IIII IIII
Qy 2221 GCGGGTTTGCGCGCGTAGGAGACGATGATTACTACGCACGTGACCAACAACAACAAGAGGT 228U H H H H H H H H H H H H H H H H H H H
QY 2161 CTGGCAGCGGTGTCCTGGTCGCTCTCCCGAGTAGGCCCGTTGTGACTGTCATGTGGGCJA 2220
GY 2101 ATTSGSCCGSGICCCCGIGGTGAGGACTCCTCAACCGGATTGGGTAAGCATGAGGTGGT3 2160 HI HIII HIII </td
GY 2041 CONCTANGOCCTIGGSCSGATGTGAGCTCSGACTCCGCCTATGGGGTGTAATTTTGGGAS 2100
GY 1981 CCATGITICTGIAGGCACTGGTTGCGGTTGTGGTTAGGCTGCACGGTTGGCAGGTTACCAA 2040 IIII-1-IIII - IIIII-1-IIII - IIIII-1-IIII IIIII-1-IIIII IIIIIIIIII
Oy 1921 TCGTTGTGGCGCCCGTGGTCCATGTGGATTGAGTGGATCAGTGTAAACCGTTGCGCG 1980
GY 1861 GOCCTATOCCGGTATGGCGCACCACGGGATCGGCAGCGTTCCGGTTGCTGGCGTGGTACC 1920
Qy 1801 TACCACTCGGTCGAGGCCCGTCACCGGCCTTCTAGCGGGTTGACCATCAGTGTTTTGCAGG 1850
QY 1741 TREGTACCESCACTARGEGGGGGGGGGAGAARCTCGGCCACCGAATCGGGATTGGGGGGAGGA 1800 H::
Qy 1581 TCACGAGATTCCTGGTCTTCCCCCAGCGTCGCGATGTCGATAGGTGTCGCGCTTTG 1740
WY 1921 AMMANDA BIOGGEOGRADICCTTTCTGGTTTTGTCTTGATGATCAAATCCGCTTCCGT 1580 Db 1697635 AAAAAGATATCGCGGCCGATCCGTTTCTGGTTTTGTCTTGATGATCAAATCCGCTTCCGT 1592694

QY 3781 AGGATGAACCCACAGCCACGGCCCGACGTTATGCCATGGCGAAGAGCGACCGGCAGGAGC 3840
Oy 3721 TECCICGEGGGAACCGGCAACAGGGACGTCGTTGCCGAAAGGGGGGGACACCGGACATCT 3780 Pb 1699735 FECCICGEGGGAAACCGACAACAGGACGTCGTTGGCGAAAAGGGCGCTGGGCACCGACACCT 1699794
2y 3661 CSANACGGIAGCAGAGGCCCATGGITGCCAACGCGGTCGCCGGGCAGTCIAGACCGGATC 3720 .il :
Qy 3501 GTCACGCCACGCGCAACACTCCGGGGGGTCGCTTCATCTGGATTCTCCTCGGTTCTGCG 366C
Oy 3541 OCCAGOATCAGGGTGCGCTCGGATTGGGAGCCGAFAGGCGGCTCCGGGCTCGGGCTCGCG 3600
Qy 3481 IAGCACTGACTGAGGGGTAGGGGGTGGCGGGGGGGGAGAGGAGGAGAGAGGGGGGGG
UY 3421 CCCCAATCAACCCAACAGTCCCCAAGGCACACAAGAAGAGTGGAAAGAAGTGCAACGCCC 3480
Qy 3361 TSAATCCCGGCGGCGGCGACCATGCCGTAGLCGCTGAAGCAGIGCGACCGATAITCATG 342C
CY 3301 GCAACCGCGCTCGGCTGGTAATCGSCGGGTAGGGAGCCARGTAGTCGGGGGGGGATTGGGT 3360 HPTHFFFHT FHT FHT FHT FHT FHT FHTH FHTH
@y 3241 CCCAGCCAATGSCTGSTAGTCGGAAAATCGCATACGGTATGCGSGCGGSGGCCCATGCA 3300 "HTT: THT: THT: THT: THT: THT: THT: THT:
CY 3181 GGAGATATGAGGGGCATGGTTAGGGGGGAGGTAAGAGAGAG
ST 3121 AGTSTSAGGAAGATGAGGACTOTOTOGAGATGGGGGTGGGGTGGGG
29 3061 ACGAACICTUTCGAGTTGCCTCGAGTGACCCCCACGCGGGGGATGACCGGGGGCCC 3120 (HT HT HT HT HT HT HT HT
6y 3001 STGGCDAGGCGACCGCTGTCSSGACAACGCCAGGAAGTAAGCCAGGGGGGATCGGTACC 3060 THITTHITTHITTHITTHITTHITTHITTHITTHITTHI
Gy 2941 AAUANGAUGGGGAGAACGANGAACTGGGGGTICACCASGAGGGGGGAAGATCACCGTGATG 3590 UH 11 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 UB 1698955 AACAGGAGGAGGAGAAGGAAGGAAGGTGAGGGTTTAACGAGGAGGGGCAAGATCACGGTGATG 1699314
Qy 2881 TIGGACACCACGACGGGGGGGGATACCAGACGACACAGTGGGGATGGGAGGGGGCAAC 2540
Qy 2821 TGGATGGACTGTGGGAICGTGCCCGGGGAAGCCTCGTGGCCACAACAGAAAGGCTGCGATA 2885 - - - - - - - - - - - -
Cy 2761 AAGGACACGITCCGCGGGGCTCTGAAGGCCCICCGAACGAACTAITGAACTTGATGATGATGCC 2820 Db 1698775 AAGGACACGITCCGCGGGTCTCGAAGCCCICCGAACCAACTAITGAACTTGAACTTGATGCCG 1698834
DE 1698715 GEGARCTIGGCCGATTGATAGTTCITGATGCTATCEGGGATCAGCAGGAGTGCCTTGCCA 2769 [1:1:111 1:111 1:111 1:11 1:111 1:111 1:111 1:111 1:111 1:111 1:11

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Db 1700755 CACCAAAGAGCTGACATGCCGGGTGATGCGACATGCGATGGGCAATACGGGCATTAGGG 1700814
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DE 1700335 CGAGGCCCGATTTGCACGCGACTGGCTGTCCGAGGACCTCGCGGGTTGCCTGTCGGTGC 1700394
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Db 1700155 TATCAGTAITGGGGCGTTCCGGCCAACGGGCTACGAGCGCGCAATGGGCTGTT 1700214
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                                              4861 TGCGGCSAAGGATGCGACGCTGACCTTGCGCCTTGCACCGTGCAATGTTGGTATGGATGCT 4920
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OY 1021 CTSCANATOGOATTCAATAGACGCCTGITGACTAAGAAAAATTCGITGTCGTGTICTCG 1689
55 J697035 CTGCAAATCGCATTCAATAGACGCCTGITGAGTAAGAAAAATTCGITGTTGTTCGT 1697834
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#594691 OSGLOGOGISOORICOSAGORISOORIAGAGORISOORIVATAOARSIOOLOGOGISOORICO GAGAAT QO
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                                                                                                                                                                                                                         1141 AATFOTAGTGCCGCCCAGTGCGCCTTTCGCCCAATGGCTCGCGTCGATCAGCGTCGCACGT 1250
                                                                                                                                                                                                                                                                                                                                               1501 GC1CGCGAAGGCCAGGATGGGCCGGACCCGGGGGCGTGCGGTGCGCGATGAACGTCGCAT 1560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 1321 AUGAIGAATTCATCGACGAATADAATCAGGTCAAAATKICCTCGCCAAGGTATGTAATTT | 1386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1261 SIGGTTITGATCSGATTTSTGTTTSGCCAATCACGCTTGGTAIATTGCATGTCATCATAG 1320
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2646 16985 54	2581 ASCAACACAARCCCACCATGACASGCGGGATACGGGGTCCGAGGGCCAGGACACGGGGCCACGACGACGACGAGGACGGGGGAGGGGGG	वव 48
2580 1698594	25.21 GGCAAGACGAAAACGAGATASTAGAAGGCGACGTCCGCGGGGGAGAAGGTGGCGGTGGGG H-LIHILLHIILLHIILLHIILLHIILLHIILLHIILLH	4a 7o
2520 1698534	2461 TREFIGANTATICCEARCACEANGAGENCECTTEGGGTCTCGGGCTACCAGTECAGCGATT	Qy da
2460 1698474	2491 GCCACGGCCAAACTCACGCAGACCCCGACCGGCGCGGGGGGGG	qu Ac
2400 1698414	341 TGTCCATAGASCGGCACGTAGAACGGCTGGCCCGGGACCGTGACGATGCTCAGC	da da
2340 1698354	231 GCCCATGTCACCGTGGTGAAAACGAGTGGCGGGTGGTACCGACTACCCCTTTGGCTCCCAGC 	90 45
2280 1698294	ZZI GCGGGTTTGCGCGGGTAGGAGACGATGATTACTACGCACGTGACCAACCA	4c &&
2220 1698234	2161 01960A300GTGTCCTGGTCTCCCGAGTAGGCCCGTTGTGACTGTCAFCTGAGGAGGA (III)	ad Ao
2160 1698174	2101 ATTGGGCCGGTGCCGGGGTGAGGACTCCTCAACCGGATTGGGTAAGCATGAGGTGGT Fill Fill Fill Fill Fill Fill Fill Fil	43
2100	2041 CCACTGASCCCCTSGCCGGAISTGASCICGGACICCGCCTATGGGGIGTAAIITTGSCAG CLHUSHUSHUSHUSHUSHUSHUSHUSHUSHUSHUUSHUUSH	40 40
2049 . 1698054	1981 CHATGITGIGTAGGCACTGGTTCGGGTTGTGGTTAGGCTGCACGTTGGCAGGTTACCAA 	ad Ac
1980 1697994	21 TOGTIGTOGCGCCOTGGICCATO	Qy dd
1920 1697934	861 GCCCTATCCCGGTATC - - 	9 <i>c</i>
1860 1697874	801 1 7815	QY Db
1800 . 1697814	1741	م ر بن
1740	1581 TCAOGAGAICGAINTECTGGTCTTCCCCCACGGTGGGGAIGTGGGAIAGGTGTCGCCCC 	9 <i>0</i> 40
1680 1697694	1921 AAAAAGATATESSOGGOGGATCOGTTTTGTCTTGATGATGATGAACCGGTTCGGT -	DB 43

OY 2641 ACSACTATSACTAGGACAGCAGCAACCCGATCTGCGTGCGTGCGAGCAGTGAGGAAACCCTCT
b 169865 ACSACTATGACTAGGACAGCAAACCCCGATCTGCGTTGCGCGGCCAGTGAGGAAACCCCG
b 169865 ACSACTATGACTAGGACAGCAAACCCCGATCTGCGTGCGGACCAGTGAGGAAACCCC

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Db 1698715 GGGATCTTGCCCCGATTGATAGTTCTTGATGCTATCGGGGATCAGCAGGAGTGCCTTGCCA 1698774
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DE 1699195 GGAGATATGACCGCCATCGTTAGGGCGACCAGGTAACAGATCAGCCCCAAGCGCGCGA 1699254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DE 1699315 GCAACCGCGTCGCCTGCTAATCGGCGGGTAGCGAGCAGCAGGTAGCCGCGGGATTGGGT 1699374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 1699435 CCCCAATCAAGCCAACAGTCCCCAGGUACTACCAAAAGAGTGGAAAAGACGTCGACCGCC 1699494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 1699495 TACCACTGACTGAGGGCGTAGGCGGTCGCCGAAATCACCGACGCAGGAGGAGGTG 1699554
                                                                                                                                                                                                                                                                  Db 1699615 GTCACGGCACCGGGCAACACCTCCGGGGGGTCGCTTCATCTGGATTCTCCTCGGTTCTGC3 1699674
                                                                                                                                                                                                                                                                                                                                                                        DB 1699555 CCGAGCATGAGGGTGCGCTCGGATTGGGAGCCGATCGCCCAGAGCCGCTCCCGCCTCGCC 1699614
                                                 Db 1699735 TTCCTCGTGGCAACCGACAACAGGACGTCGTTGCCGAAAGGGCGCTGGGCACCGACATCT 1699794
                                                                                                                                                            1699675 CGAAACGGTAGCAGAGCGCCATGGTTGCCAACGCGGTCGCCGGCCAGTCTAGACCGGATC 1699734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2791 GGGATCTTGCCCGATTGATAGTTCTTGATGCTATGGGGGATCAGCAGGAGGAGGGCTTGGCA 2760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2821 TGGATCGACTGTGCGATCGTCCCCGGGAAGCCTCGTGGCCACAACAGAAAGGCTGCGATA 2880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3061 ACGAACCCTGTCGAGTTGCCTCGATCGATCACCCCCACGCCCGGGATGGCCCGGCGGCGCC 3120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2941 AACACCACGCCGAGAACGACGACTGCGGCTTTACCAGGACGGCCAAGATCACCGTGATG 3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3181 GGAGATATGACCGCCATCGTTAGGGCGACCAGGTAACAGATCAGCCCCCAAGCGCGGGGA 3240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3301 GCAACCGCGCTCGGCTGGTAATCGGCGGGTAGCGAGATCAGCTAGTCCGCGGGGATTGGGT 3360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3121 ACTSTCACGAAGATGACCACTCGCTCCAGACCACGTGCCCCCGGGGCCGCCCAGAIGGCG 3180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3421 CCCCAATCAAGCCAACAGTCCCCAGGGACTACCAAAAGAGTGGAAAAAGACGTCGACCGCG 3480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3481 TACCACTGACTGAGGGGGTACGCCGTUGCCGCCGAAATCACCGACGCCAGCAGGATGGTG 3540
                                                                                                     3721 TICCTCGTGGCAACCGACAACAGGACGTCGTTGCCGAAAGGCCGGTGGGCACCGACATCT 3780
                                                                                                                                                                                                           3661 CGAAACGGTAGCAGAGCCCCATGCTTGCCAACGCGGTCGCCCGGGCAGTCTAGACCGGATC 3720
                                                                                                                                                                                                                                                                                             3541 CCGAGCATGAGGGTGCGCTCGGATTGGGAGCCGATCGCCCAGAGCCGCTCCCGGCTCGCG 3600
3781 AGGATGAACCCACAGCCACGCCCCGACGTTATGCCATGGCGAAGAGCGAACCGGCAGGAGC 3840
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Db 1699855 GGGAACCCAGTGAAGCGAGCGCTCATCALCGGAATCACAGGACCGGGACGGCTCGTATLTC 1699914
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DB 1700155 TATOKGTATTGGGGCCTTCCGGGCAGGGGAGGGGAGGGGGGAGGGGGGGAATGSGTGTT 1700224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DU 1700755 CACCAAAGAGCTGACATGCCGGGTGATGTGACATCGCATGGAGGGCAATACGGGCATGGA 1700814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SP 1790695 CITCCISTGCCCGAATTACGTATTCCCGTACGAACCGCATTTCAATATCCCAACALICTT 1300754
                                                                                                                                                                                                              THE TRACE TRACECOAAGGASTETGGCGTTCGCTCAACTGATTACGGTTCCCCAAGGTGAAACGGCTT 1790874
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                486) TGACCCGAAGGCCTGGCCTTCGCTTAACT3GATTACGGTTCCCAAGGTGAAACGCT1 4869
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Db 1703215 CGACCCGCACCAACCGGGCGCGCGCGCTGTTCTGCACTATGGTGACCTGATCGACGGAAC 1753274 --DE 1703335 GTCACACGTGCGGGTGAGCTTCGACGAACCCGTGCACACCACCGGCATGGG 1703354 Db 1703575 CGAAGCGTACGGATTGTTCGCCGTTAACGGCATCTTGTTCAATCACGGAATCACCGCGGGG 1703634 οy OY 7741 ATACGTCGAAGGCAIGTGGGGGATGGTGCAGACCGACGAGCGAGGAGTTCGTITTUGG 7830
DE 1703755 ATACGTCGAAGGCATGGGGGGTGCTGCAGACGACGACGACGACGACGACGACGACGATGTTTGGC 1703814 Oy 7801 GACCGGGGGTTTCACCGTGAGTTCGCGGGGGGGGGGGGTTCGAGCATGCGGTTT 7869 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 11 OF 7861 GRACTGGCAGCAGTACGTGAAATTCGACCGACGGTATCTGCGGGGCCACCGAGGTGGATTC 7920
DE 1703875 GGACTGGCAGCAGTACGTGAAATTCGACCGACGCTATCTGCGGCCCACCGAGGTGGATTC 1703534 Db 1703935 GCTGATCGGCGACCGACCAAGGCTGCCGAATTGCTGGGCTGGAGGGCTTCGGTGCACAC 1703954 DE 1704115 CCCCTTGACCGCGCCCCGGGTCTACATCGCCGGGCATCGCGCCTGGTCGGGTCCGCG 1704174 7261 CCGGTTGGTGACCCTGCTGAGCACCATCGAACCCGACGAGGTGTACAACCTGGCCGCGA 7320 7201 CGACCCGCACCAACCGGGCGCGCGGCTGTTTCTGCACTATGGTGACCTGATCGACGGAAC 7260 7321 STCACACGTGCGGGTGAGCTTCGACGAACCCGTGCACACCGGTGACACCACCGGCATGGG 7380 7621 CGGTGAGACGTICGTGACCCGAAAGATCACCAGGGCCGTGGCACGCATCAAGGCCGGTAT 7680 7981 TGACGAGTTGGCTCGGATCATGGTCGACGCGGACATGGCGGCGCTGGAGTGCGAAGGCAA 8040 8101 CCGCTTGACCGCGCGCGCGCGGGTCTACATCGCCGGGCATCGCGGGCCCTGGTCGGGTCCGGG 8160

8161 CIGCTACGCACGITTGCGGGCGCGGGGTTCACCAACCTGCTGGTGGGGGTCACGCGCGAG 8220

Db 1704295 GTCATCGACGGGGGGCCGGGGTCGGCGGCATCCTGGCAACGACGACACCTACGCGGGCGAT 1704354 8281 GTCATCGACGCGGGGGCCCCGGGCGGCATCCTGGCCAACGACACCTACCCGGCCGAT 8340

Db 1704535 GCCAAAATCGCCGGCATCCTTGCGGTCCAGGCGGTGCGCTGCCCAACATGGCCTGCGTGG

8521 GCCAAAATCGCCGGCATCCTTGCGGTGCAGGCGGTGCGCCCAACATGGCCTGCCGTGG 8580

pb 1704595 Arcicedocarreceaceaecersiaecescadeciacaaecrificadeciacacertes 1704654

8581 ATCTEGGCGATGCCCACCAACCTGTACGGGCCAGGCGACAACTTTTCGGCGGTCGGCGTCG

TOWARDS GTOACCAACTGGGGACCCGGCACGCCGGACGGGACGTGGACGTCGACGTGGACCT3GGG 1764774

8701 GTGACCAACTGGGGGACCGGCACGCCCGGACGGGGGGGACGTGCACGTCGACGACCTGGGG 8760

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906) CTCGGAACATCITGCGTCGCAACGGCAICGGGIJTCGCGGTACTIIGCCGAACIGGACT 9120

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9121 GGGAACGCAATTTCYTGCGCCAACTGCAATCGCATCGGGTCAGTGCCGTGCTCGATGTCG 9180

DE 1704275 ACCUCATGCCIGTATCIGCTGGAAMATITCGACGAGGGAACGAACGTGAAACGTGGGAAACC 1204834

DE 1704655 CATCIBOTOCOGCACTOCATOCOCCUSTTATBACGAGGCCAAAGCCAGIBGCGGGCCGAAC 1704714

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UY 9361 TOGCOGGAACGAGGGCGCCAGCAGTTCCGTCTTGCCGATGTTSAAACGACATCAGGACS 9420
Db 1795375 TCGCCGGCAACGAGGGCGCCAGCAGTTCCGTCTTGCCGATGTTGAAACGACATCAGGACS 1795334
OY 18321 ACAGATCACCGATGCGTGGGGGATGCCCTGGTTCATCGCGTGGTACCGCGGCGTCGG 19380
Db 1706335 ACAGATCACCCGATGCGTGGCGTGGTTCATCGCGTCGTACCGCCGCGCGTCGG 1796394
                                                                                                                                                                                                                                                                                               Db 1706215 CGAGACGATCCGTAAGCCCCACAATTCGGACACGGTCCCTTGCCGGATAGCGCCT 1706274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 1706095 CACCGATCTTGGCCAGCGATGATCCGAAGAACGATGCTTGATGCGGAACAACCTGCT 1706154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db 1706035 CCAGCGCGGCCCGCAATATGAATTCCTGGTCGGCGGCGATCCCGAAATCAAGGTCGTAGC 1708034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35 1795915 GCCATCAAGGTCGCCCATGCCGCACATCACCGCAAGAACCCCCCTTGGTTACCCGCGCTCGCC 7755974
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 1706155 TGCCGGCCAGGAATTTGCGCAGGCTGAAAGGTATCGGGCCGCGCACCCGATCGAGCCCGA 1706214
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                                                                                                                                                 Dh 1706275 CCACGGCCTGGGCTACCACGTCGGGCCCGGAAAAACGATCGGCGGGGGTGCAAGAACCACA 1756334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1705735 GCAACGGTCGAATGCTGCAGGCCGATGGCATCTTCTTCCGGGGGAAGGGAATGACGCGCCG 1705794
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                                                                                                                                                                                                                                                                                                                         10201 GGAGACGATCCATCCCGAAGCCCCACAATTGGGACAACCGGTCCCTTGCCGGATAGCGCCT 15260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10021 CCAGCGCCGCCAATAIGAATTCCTGGTCGGCGGCGATCCCGAAAICAAGGTCGTAGC 10080
                                                                                                                                                                                                                    19261 CCACGGCCTGGGCTACCACGTCGGGCCCGGAAAAACGATCGGCGGAGTGCAAGAACCACA 10320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10081 CACCGATCTTGGCCACCAGCGATGATCCGGAAGAACGATGGTTGATGCGGAACAACCTGCT 10140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9651 ATCTCGTGGATTCGTTGGGCTTTACGCTCTCGGGATTGCAACCGGGTTTCACCGACCCCC 9720
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Qy (116) GGCAGGTTGGATGTSGATGTAGTAGTAGAGGCGCCALGTTCAGGTGGCGAAGCTCG (1220) H ...H: H ...H: HH ...H. ...H OY 10921 OSOCSCAGCAGOGATCGGTENACTIGTCSTSCGTENTGGTENACCGGRASCGGASCCATTTATOG 1098: HTH 1.111 HTT.111 HTT.11 HTT.111 HTT.11 H DE 1706635 SICTEGATACCSATGAGGGTGCGTGGAGGATICGGCGGGATAGGGAACCTCCGAGGAACGAC 1706694 DE 1707235 ATCCCGAGGACCTGAAATCCCATGCGCGCGAACCCGACTACCGCCTTCCAACCAG 1707294 ED 1707055 AGGGTTTCCNCGTATTCCTTCCGARTCTCCAGGTCGTAGAAGAGGCCGCAGGAAAAGACG 1707114 8 Db 1706575 GUSTCOUAGCAGAAGGTCACCGAGTTCCCCTAGGTTCCTGGCGGGGGGATCACCGG 1706634 1707295 CCGACATCGGCCAGGCGTAGGTGGCTCTTGTCCCCGGGAAAGACGGTTTCCAGAAATCCCG 1707354 1756755 TIGATGGCCTGAAGIAGTIOTCGCGTGGAATCAAGAGTGACGGGGGATTGTOCCAGGAACTAGC 10621 GLOTTGALAUGGATGAAGGTTGCCTCGAAGALLGGCGGCATAGGAACCLCCGAGCAACGAC 10680 10741 TTSATGGCCTGAAGIAGGTCCCTTCGAAICUAGAATJACCGCCGATTGICCCAAGAC 10900 19561 CGGTCGGAGCAGACGTGACCGAGTTCCCCTAGGTTSCTGGCGGCGATTGTGGATCACCGG 19620 11281 CCGACATEGOCCAGGCGTAGGTGCCTUTTGTCCCCGGGAAAKSACGGTTTCCAGAATCCCG 11346 11221 ATCCCGAGGACCIGAAATCCCATGCGCGCGAAACCCGAACGAGCCGGCCTTCCAAGAG 11280 10441 GGGGGTGGGATTAGATTGGTGGTGGATGGGTGGGGGTAGGGTTAGGGTAGGGTAGGTAGGGTAGGGTAGGGTAGGGTAGGGTAGGGTAGGATAGAA

11401 GITCCGTCUTCGAGGCGAACGITGTGGGGCGGTGAATTGTACCGGGCCGAACGTTCC

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QY 12241 AGGGACGTACTOGCCGCGAGCGGCGACCAACGGCGCGGCTCAGGTTCCCATTGAGGCCGA 1230C FF 1708255 ACGCGACGTACTCGCCGGGGGGGGGCGGAGAGGGGCCCGGTCAGGTTCCCATTGAGGCCGA 1708314
                                                                                                                                           DE 1708375 TOATCOCCOSCISCICATION (1117) (1117) (1117) (1117) (1117) (1117) (1117) (1117) (1117) (1117) (1117)
                                                                                                                                                                                                                                                                                                                                            Sb 1708195 GGANTGCGACCCCTTTGCTTAGCTTCAGCAGATCCATCAGTAGTCGTCGCCTCGCCACA 1708254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fb 1708135 CCTCCTCCCATATCACTCSGACCSSATGGAAGCACACCGTCSTCTTGGGGTGCCGGTCSA 1708194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 1708015 ASCRETEGARGEGRACGSTACACGRECORGITEGTCISGAIGAAGTICATCAAGAICAACC 1708774
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1707715 CCTCCGGGCCIGGAACGTTGGCGATCIGGCGAAGGATCCAGTCGGCCAIGACGGCGATGA 1707774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12181 GGAATGOGACOTGTTTGCTTAGCTTCAGCGGATCGATCCAGTAGTCGTCCGCCTCGCACA 12240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11921 GCCCCGGACCCTGGGTCAACCAGAACTTGGGGGGTCCACCACCTGGTTGTGGCCACATGC 11880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11761 GCTCCTCGCGCGCGCGCGTCTCCCGGGAACAGGTCGAGCATCGCGTCAAACGTCGCCGCAT 11820
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                                                                                               12481 TGGTCGAGACGATGCTCACCTIGGGGCAAAGCIGGGGACTCACCGTCGGGCCTTTTCCTG 12540
                                                                                                                                                                                                                                                                                             12361 TONFOSCOSSIGNESCATOSSITOSACESSITOSITOSCOSACEATORICITOSACOSGEAAGI 12420
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KEYWORDS
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Db 1708675 ACTGACGTIGGGCTCGAACCGCGTGGCGCGGGTGTGGGCGCACCGTCTCGAGICGGTGC 1708734
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Mycobacterium tuberculosis CDC1551
Bacteria: Firmicules: Actinobacteria: Actinobacteridae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (25-APR-2001) The Institute for Genomic Research, 9712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium: Mycobacterium tuberculosis complex 1 (bases 1 to 4403836)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
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                                                                                                                                                      PATDEADUTTVPPSENPATTSPOTTTONDEIDDSAAARGDNQHSHPSYFTERPHNIDS
ATAGVTSLNRRYTFDTFVIGASNRFAHAAALA LAEAPARAYNP:,FIWGESG!;GKTHLL
HAAGNYAQRLF PGMRVKYVSTEELTNUFINSLRDDRKVAFKRSYHDVDVLLVDDIQFI
SSKEGIGEEFFHIERILHANNKOIVISSDRPKOLATLEDRLÆTRFERGLITEVOPPE
LEIR AI IRKKAOMERLAVPDDVIEL, ASSI PRNIFELEGALIKVIRARSLIKKIP DIK
ALREIVLRDLIADANTWOLSAATINAARAEVFETTVEELRGRKITRALACSROIAWYL
SRELIULSLPKIGGAPGROHTTVMYAORKILSEMAERREVEDHVKELITRIRORSKR*
                                                                                                                                                                                                                                                                                                                                                                /transl_table=11
/product "chromosomal replication initiator protein DnaA"
/protein_Id=AAK44224 ["
/db_xref="Gril3879042"
                                                                                                                                                                                                                                                                          RAWLNLVQPLTIVEGFALLSVPSSFVQNE1ERHLRAPITDALSRKLGHQIQLGVRIAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"similar to SP:P46388 PID:886325 PID:1262352
identified by sequence similarity: putative"
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                                                                                                                                                                                                                                                                                                                     /translation-^MTDDPGSGFTTVWNAVVSELNGDPKVDDGPSSDANLSAPLTPQQ
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